

GenCore version 4.5
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On nucleic - nucleic search, using sw model

Run on:

December 3, 2000, 10:15:26 ; Search time 10069.4 Seconds
(without alignments)
3236.486 Million cell updates/sec

Title:

US-09-227-881-34

Perfect score:

5271
1 atcttttgttcagtttaactc.....tggggatgagccagcagg 5271

Sequence:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Scoring table:

7189864 seqs, 301403243 residues

Total number of hits satisfying chosen parameters:

14379728

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

10: gb_est10:*

11: gb_est11:*

12: gb_est12:*

13: gb_est13:*

14: gb_est14:*

15: gb_est15:*

16: gb_est16:*

17: gb_est17:*

18: gb_est18:*

19: gb_est19:*

20: gb_est20:*

21: gb_est21:*

22: gb_est22:*

23: gb_est23:*

24: gb_est24:*

25: gb_est25:*

26: gb_est26:*

27: gb_est27:*

28: gb_est28:*

29: gb_est29:*

30: gb_est30:*

31: gb_est31:*

32: gb_est32:*

33: gb_est33:*

34: gb_est34:*

35: gb_est35:*

36: gb_est36:*

37: gb_est37:*

38: gb_est38:*

39: gb_est39:*

40: gb_est40:*

41: em_estba:*

42: em_estfun:*

43: em_esthun1:*

44: em_esthun2:*

45: em_esthun3:*

46: em_esthun4:*

47: em_esthun5:*

48: em_esthun6:*

49: em_esthun7:*

50: em_esthun8:*

51: em_esthun9:*

52: em_esthun10:*

53: em_esthun11:*

54: em_esthun12:*

55: em_esthun13:*

56: em_esthun14:*

57: em_esthun15:*

58: em_esthun16:*

59: em_esthun17:*

60: em_esthun18:*

61: em_esthun19:*

62: em_esthun20:*

63: em_estin1:*

64: em_estin2:*

65: em_estin3:*

66: em_estin4:*

67: em_estin:*

68: em_estov1:*

69: em_estov2:*

70: em_estol1:*

71: em_estol2:*

72: em_estp13:*

73: em_estp14:*

74: em_estp15:*

75: em_estrol1:*

76: em_estro2:*

77: em_estro3:*

78: em_estro4:*

79: em_estro5:*

80: em_estro6:*

81: em_estro7:*

82: em_estro8:*

83: em_estro9:*

84: em_estro10:*

85: em_estrol1:*

86: em_estrol2:*

87: em_estrol3:*

88: gb_gss1:*

89: gb_gss2:*

90: gb_gss3:*

91: gb_gss4:*

92: em_gss1:*

93: em_gss2:*

94: em_gss3:*

95: em_gss4:*

96: gb_gss5:*

97: gb_gss6:*

98: gb_gss7:*

99: gb_gss8:*

100: gb_gss9:*

101: gb_gss10:*

102: gb_gss11:*

103: gb_gss12:*

104: gb_gss13:*

105: gb_gss14:*

106: gb_gss15:*

107: gb_gss16:*

108: gb_gss17:*

109: gb_gss18:*

110: gb_gss19:*

111: gb_gss20:*

112: gb_gss21:*

113: gb_gss22:*

114: gb_gss23:*

115: gb_gss24:*

116: em_gss5:*

LOCUS	AQ057239	660 bp	DNA	GSS	30-JUL-1998
DEFINITION	CIT-HSP-2340D14.TR	CIT-HSP	Homo sapiens	genomic clone	2340D14, DNA
SEQUENCE	em_gss9:*				
ACCESSION	AQ057239				
VERSION	AQ057239.1				
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 660)				
AUTHORS	Adams, M.D., Rounseley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.				
TITLE	Use of a random BAC End sequence Database for Sequence-Ready Map Building (1998)				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT
AQ057239

ACCESSION # AC0379787 LOCUS RPCI11-152C3.539 bp DNA DEFINITION Homo sapiens genomic clone GSS 20-MAY-1999

KEYWORDS		GSS.	
ORGANISM		Homo sapiens	
SOURCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;	
ORGANISM		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1 (bases 1 to 577)	
AUTHORS		Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.	
TITLE		Use of a random human BAC End Sequence Database for Sequence-Ready Map Building	
JOURNAL		Unpublished (1998)	
COMMENT		Other_GSS, CIT-HSP-2372C9.TR	
CONTACT		Department of Eukaryotic Genomics	
CONTACT		The Institute for Genomic Research	
CONTACT		9712 Medical Center Dr., Rockville, MD 20850, USA	
CONTACT		Tel: 301 838 0200	
CONTACT		Fax: 301 838 0208	
CONTACT		Email: mddam@tigr.org	
CONTACT		Clones are available from Research Genetics (info@resgen.com). BAC	
CONTACT		end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html .	
CLASS		Class: BAC ends	
FEATURES		Location/Qualifiers	
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BASE COUNT		87 a 145 c 118 g 166 t	
ORIGIN			
FEATURES		Query Match	
SOURCE		3.4%; Score 177.6; DB 89; Length 516;	
BASE COUNT		Best Local Similarity 85.2%; Pred. No. 8e-21; Matches 213; Conservative 0; Mismatches 29; Indels 8; Gaps 1;	
ORIGIN		Matches 213; Conservative 0; Mismatches 29; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
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SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
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BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
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SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
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BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
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BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
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FEATURES		Query Match	
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ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity 75.1%; Pred. No. 8.5e-21; Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
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FEATURES		Query Match	
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ORIGIN		Matches 238; Conservative 0; Mismatches 71; Indels 8; Gaps 1;	
FEATURES		Query Match	
SOURCE		3.4%; Score 177.4; DB 91; Length 577;	
BASE COUNT		Best Local Similarity	

RESULT 9
AO199435/c
LOCUS AO199435 434 bp DNA GSS 20-APR-1999

RESULT 15

Mon Dec 4 08:51:43 2000

us-09-227-881-34.rst

Page 10

Db
65 CTTGGCTGGTTGCTA 48

Search completed: December 3, 2000, 10:15:41
Job time: 14019 sec